OIPE

RAW SEQUENCE LISTING DATE: 07/18/2001
PATENT APPLICATION: US/09/758,575 TIME: 12:43:17

Input Set : A:\517.app.txt
Output Set: N:\CRF3\07182001\I758575.raw

ENTERED

<110> APPLICANT: Kaufmann, Joerg
Harrowe, Greg
Reinhard, Christoph
Kang, Sammao
<120> TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN
BREAST CANCER
<130> FILE REFERENCE: 200130.517/1656.002
<140> CURRENT APPLICATION NUMBER: US 09/758,575
<141> CURRENT FILING DATE: 2001-01-09
<160> NUMBER OF SEQ ID NOS: 10
<170> SOFTWARE: FastSEQ for Windows Version 4.0
<210> SEQ ID NO: 1
<211> LENGTH: 2366
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 1
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gccgcggagc cgggccgggg cagcgccgtc tccgcctcgg ggccgccggg ggcgccctgc 180
tgagcgctac ccacgtgcgt ccgcgccacc tcgcgggcga ccccgcggcc aaggcccccg 240
gcggagcggc tcccgggcgc cccgaactag cccccaactt tgggcgaagt ttgcctgcgc 300
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caagcccgac ggcaccctcg tctccttcac cgccgacttc aagaaggatg tgaaggtctt 600
ccgggccctg atcctggggg agctggagaa ggggcagagt cagttccagg ccctctgctt 660
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gtgtggcatc cgcagctgcc agaagagcta cagcttcgac ttctacgtgc cccagaggca 1140
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tccctcctgc atctcccctg gagtgttcac ttgcaagctg ccaaaacatg atggcctctg 1500
gttgttctgt tgaactcctt gaacgtttag accctaaaag gagtctatac ctggacaccc 1560
acctccccag acacaactcc cttccccatg cacacatctg gaaggagctg gcccctcagt 1620
cccttcctac tccccaacaa ggggctcact atccccaaag aaggagctgt tggggaccca 1680
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ggggcgagtg gagacctccc atcactgaga cagatcacag accacgagtg cctttcccgg 1800
acctggacgt tgcctccaaa acaggcacca gctctttccc tctctagaca gaaatatttt 1860

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```
61 tgtaaggttc tggggcaggg agggagcatg aagtacgagg aaaacttgaa ttccagattt 1920
62 ttaatgcaaa gtatttatca tttctaccag aaataaacgt tttaagtttt tacttgacta 1980
63 atgagaccca gagtttggag aaaacttttg gccaatgctg ccacctgatg tcagaaagtg 2040
64 tccccacacc ctagcagtgg cctatcttgg aacaagaact tcgaaagcac ctactgtgtg 2100
65 ctcagccatt tgaggaagga aggaggagaa ggaagatgtt actagggaag gatgagataa 2160
66 aacttctgca cccaagacaa tgagacagac ataactgcaa ccgtagtaag ccagtcagaa 2220
67 atagccagcg cgaaggcaag agatggggtg gagattggaa ccccgcttca gatctgggct 2280
68 cggctactta cctgctgtgc agccatgggt caagttgctt gacctctctg tgcctccact 2340
69 cccttagcta taaaatgagc ttactt                                     2366
71 <210> SEQ ID NO: 2
72 <211> LENGTH: 273
73 <212> TYPE: PRT
74 <213> ORGANISM: Homo sapiens
76 <400> SEQUENCE: 2
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79 Leu Pro Leu Leu Ala Pro Leu Leu Gly Thr Gly Ala Pro Ala Glu Leu
80             20                  25                  30
81 Arg Val Arg Val Arg Leu Pro Asp Gly Gln Val Thr Glu Glu Ser Leu
82         35                  40                  45
83 Gln Ala Asp Ser Asp Ala Asp Ser Ile Ser Leu Glu Leu Arg Lys Pro
84     50                  55                  60
85 Asp Gly Thr Leu Val Ser Phe Thr Ala Asp Phe Lys Lys Asp Val Lys
86 65                  70                  75                  80
87 Val Phe Arg Ala Leu Ile Leu Gly Glu Leu Glu Lys Gly Gln Ser Gln
88                 85                  90                  95
89 Phe Gln Ala Leu Cys Phe Val Thr Gln Leu Gln His Asn Glu Ile Ile
90             100                 105                 110
91 Pro Ser Glu Ala Met Ala Lys Leu Arg Gln Lys Asn Pro Arg Ala Val
92         115                 120                 125
93 Arg Gln Ala Glu Glu Val Arg Gly Leu Glu His Leu His Met Asp Val
94     130                 135                 140
95 Ala Val Asn Phe Ser Gln Gly Ala Leu Leu Ser Pro His Leu His Asn
96 145                 150                 155                 160
97 Val Cys Ala Glu Ala Val Asp Ala Ile Tyr Thr Arg Gln Glu Asp Val
98                 165                 170                 175
99 Arg Phe Trp Leu Glu Gln Gly Val Asp Ser Ser Val Phe Glu Ala Leu
100            180                 185                 190
101 Pro Lys Ala Ser Glu Gln Ala Glu Leu Pro Arg Cys Arg Gln Val Gly
102        195                 200                 205
103 Asp Arg Gly Lys Pro Cys Val Cys His Tyr Gly Leu Ser Leu Ala Trp
104    210                 215                 220
105 Tyr Pro Cys Met Leu Lys Tyr Cys His Ser Arg Asp Arg Pro Thr Pro
106 225                 230                 235                 240
107 Tyr Lys Cys Gly Ile Arg Ser Cys Gln Lys Ser Tyr Ser Phe Asp Phe
108                245                 250                 255
109 Tyr Val Pro Gln Arg Gln Leu Cys Leu Trp Asp Glu Asp Pro Tyr Pro
110            260                 265                 270
111 Gly
```

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Input Set : A:\517.app.txt
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<210> SEQ ID NO: 3
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Putative signal peptide
<400> SEQUENCE: 3

```
Met Arg Leu Pro Gly Val Pro Leu Ala Arg Pro Ala Leu Leu Leu Leu
 1               5                  10                  15
Leu Pro Leu Leu Ala Pro Leu Leu Gly Thr Gly Ala Pro Ala
            20                  25                  30
```

<210> SEQ ID NO: 4
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Anti-sense oligonucleotide
<400> SEQUENCE: 4

```
agctgcggat gccacacttg tagg                                          24
```

<210> SEQ ID NO: 5
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Reverse control oligonucleotide
<400> SEQUENCE: 5

```
ggatgttcac accgtaggcg tcga                                          24
```

<210> SEQ ID NO: 6
<211> LENGTH: 273
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 6

```
Met Arg Leu Pro Gly Val Pro Leu Ala Arg Pro Ala Leu Leu Leu Leu
 1               5                  10                  15
Leu Pro Leu Leu Ala Pro Leu Leu Gly Thr Gly Ala Pro Ala Glu Leu
            20                  25                  30
Arg Val Arg Val Arg Leu Pro Asp Gly Gln Val Thr Glu Glu Ser Leu
        35                  40                  45
Gln Ala Asp Ser Asp Ala Asp Ser Ile Ser Leu Glu Leu Arg Lys Pro
    50                  55                  60
Asp Gly Ile Leu Val Ser Phe Thr Ala Asp Ile Lys Lys Asp Val Lys
65                  70                  75                  80
Val Phe Arg Ala Leu Ile Leu Gly Glu Leu Lys Lys Gly Gln Ser Gln
                85                  90                  95
Phe Gln Ala Leu Cys Phe Val Thr Gln Leu Gln His Asn Glu Ile Ile
            100                 105                 110
Pro Ser Glu Ala Met Ala Lys Leu Arg Gln Lys Asn Pro Arg Ala Val
        115                 120                 125
Arg Gln Ala Glu Glu Val Arg Gly Leu Glu His Leu His Met Asp Val
```

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```
175     130                 135                 140
176 Ala Val Asn Phe Ser Gln Gly Ala Leu Leu Ser Pro His Leu His Asn
177 145                 150                 155                 160
178 Val Cys Ala Glu Ala Val Asp Ala Ile Val Thr Arg Gln Glu Asp Val
179                 165                 170                 175
180 Arg Phe Trp Leu Glu Gln Gly Val Asp Ser Ser Val Phe Lys Ala Leu
181             180                 185                 190
182 Pro Lys Ala Ser Glu Gln Ala Glu Leu Pro Arg Cys Arg Gln Val Gly
183         195                 200                 205
184 Asp Arg Gly Lys Pro Cys Val Cys His Tyr Gly Leu Ser Leu Ala Trp
185     210                 215                 220
186 Val Pro Cys Met Leu Lys Val Cys His Ser Arg Asp Arg Pro Thr Pro
187 225                 230                 235                 240
188 Val Lys Cys Gly Ile Arg Ser Cys Gln Lys Ser Tyr Ser Phe Asp Phe
189                 245                 250                 255
190 Val Val Pro Gln Arg Gln Leu Cys Leu Trp Asp Glu Asp Pro Tyr Pro
191             260                 265                 270
192 Gly
196 <210> SEQ ID NO: 7
197 <211> LENGTH: 332
198 <212> TYPE: PRT
199 <213> ORGANISM: Drosphilia melanogaster
201 <400> SEQUENCE: 7
202 Met Ile Leu Lys Glu Glu His Pro His Gln Ser Ile Glu Thr Ala Ala
203  1               5                  10                  15
204 Asn Ala Ala Arg Gln Ala Gln Val Arg Trp Arg Met Ala His Leu Lys
205             20                  25                  30
206 Ala Leu Ser Arg Thr Arg Thr Pro Ala His Gly Asn Cys Cys Gly Arg
207         35                  40                  45
208 Val Val Ser Lys Asn His Phe Phe Lys His Ser Arg Ala Phe Leu Trp
209     50                  55                  60
210 Phe Leu Leu Cys Asn Leu Val Met Asn Ala Asp Ala Phe Ala His Ser
211 65                  70                  75                  80
212 Gln Leu Leu Ile Asn Val Gln Asn Gln Gly Gly Glu Val Ile Gln Glu
213                 85                  90                  95
214 Ser Ile Thr Ser Asn Ile Gly Glu Asp Leu Ile Thr Leu Glu Phe Gln
215             100                 105                 110
216 Lys Thr Asp Gly Ile Leu Ile Thr Gln Val Ile Asp Ile Arg Asn Glu
217         115                 120                 125
218 Val Gln Ile Leu Lys Ala Leu Val Leu Gly Glu Glu Lys Arg Gly Gln
219     130                 135                 140
220 Ser Gln Tyr Gln Val Met Cys Phe Ala Thr Lys Phe Asn Lys Gly Asp
221 145                 150                 155                 160
222 Phe Ile Ser Ser Ala Ala Met Ala Lys Leu Arg Gln Lys Asn Pro His
223                 165                 170                 175
224 Thr Ile Arg Thr Pro Glu Glu Asp Lys Gly Arg Glu Thr Phe Thr Met
225             180                 185                 190
226 Ser Ser Trp Val Gln Leu Asn Arg Ser Leu Pro Ile Thr Arg His Leu
227         195                 200                 205
```

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228 Gln Gly Leu Cys Ala Glu Ala Met Asp Ala Thr Val Val Arg Asp Val
229 210 215 220
230 Asp Leu Lys Ala Trp Ala Glu Leu Pro Gly Ser Ser Ile Ser Ser Leu
231 225 230 235 240
232 Lys Ala Ala Thr Glu Lys Phe Pro Asp Thr Leu Ser Thr Arg Cys Asn
233 245 250 255
234 Glu Val Ser Ser Leu Trp Ala Pro Cys Leu Cys Asn Leu Glu Thr Cys
235 260 265 270
236 Ile Gly Trp Val Pro Cys Gly Leu Lys Val Cys Lys Gly Lys Gly Val
237 275 280 285
238 Ala Gly Ala Asp Ser Ser Gly Ala Gln Gln Gln Ala Gln Pro Thr Asn
239 290 295 300
240 Val Arg Cys Gly Ile Lys Thr Cys Arg Lys Cys Thr Gln Phe Thr Tyr
241 305 310 315 320
242 Val Val Arg Gln Lys Gln Gln Cys Leu Trp Asp Glu
243 325 330
246 <210> SEQ ID NO: 8
247 <211> LENGTH: 2366
248 <212> TYPE: DNA
249 <213> ORGANISM: Homo sapiens
251 <400> SEQUENCE: 8
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253 gacgggggt gggattgaat gaaaagtgca aaacacaggc tcgcagcgct ggagcccggg 120
254 gccgcggagc cgggccgggg cagcgccgtc tccgcctcgg ggccgccggg ggcgccctgc 180
255 tgagcgctac ccacgtgcgt ccgcgccacc tcgcgggcga ccccgcggcc aaggcccccg 240
256 gcggagcggc tcccgggcgc cccgaactag cccccaactt tgggcgaagt ttgcctgcgc 300
257 ctctccccgc ccccacgcgg cgcgccgggg ccgcggacgg cagcggcccc cggggatgcg 360
258 ccttcccggg gtacccctgg cgcgccctgc gctgctgctg ctgctgccgc tgctcgcgcc 420
259 gctgctggga acgggtgcgc cggccgagct gcgggtccgc gtgcggctgc cggacggcca 480
260 ggtgaccgag gagagcctgc aggcggacag cgacgcggac agcatcagcc tcgagctgcg 540
261 caagcccgac ggcaccctcg tctccttcac cgccgacttc aagaaggatg tgaaggtctt 600
262 ccgggccctg atcctggggg agctggagaa ggggcagagt cagttccagg ccctctgctt 660
263 tgtcacccag ctgcagcaca atgagatcat ccccagtgag gccatggcca agctccggca 720
264 gaaaaatccc cgggcagtgc ggcaggcgga ggaggttcgg ggtctggagc atctgcacat 780
265 ggatgtcgct gtcaacttca gccaggggc cctgctgagc ccccatctcc acaacgtgtg 840
266 tgccgaggcc gtggatgcca tctacacccg ccaggaggat gtccggttct ggctggagca 900
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268 tcgctgcagg caggtggggg accgcgggaa gccctgcgtc tgccactatg gcctgagcct 1020
269 ggcctggtac ccctgcatgc tcaagtactg ccacagccgc gaccggccca cgccctacaa 1080
270 gtgtggcatc cgcagctgcc agaagagcta cagcttcgac ttctacgtgc cccagaggca 1140
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273 gccttatttc cctccctccc cactcccctg gccctagagc ctgggccccc ctggccccat 1320
274 ctcacatgac tgtgaagggg gtgtggcatg gcaggggtc tcatgaaggc acccccattc 1380
275 ccaccctgtg ccttccttgc gggcagagag ggagagaagg gctccccaga tctacacccc 1440
276 tccctcctgc atctcccctg gagtgttcac ttgcaagctg ccaaaacatg atggcctctg 1500
277 gttgttctgt tgaactcctt gaacgtttag accctaaaag gagtctatac ctggacaccc 1560
278 acctccccag acacaactcc cttccccatg cacacatctg gaaggagctg gcccctcagt 1620
279 cccttcctac tccccaacaa ggggctcact atccccaaag aaggagctgt tggggaccca 1680

VERIFICATION SUMMARY DATE: 07/18/2001
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